

1. The first step is to identify the problem. This involves understanding the current situation and the goals that need to be achieved.

(1) GENERAL INFORMATION:

(i) APPLICANT: Soppet, Daniel R  
Yi, Li  
Rosen, Craig A  
Ruben, Steven

(ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
HLTDG74

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.  
(B) STREET: 9410 Key West Ave  
(C) CITY: Rockville  
(D) STATE: MD  
(E) COUNTRY: USA  
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/468,011  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: PF201D1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2003 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 90..1712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GT TTGCTCTG GGCAGCCAAG TTGGCATATT GGAAGCTTTT TCCGGGCTCT GGAGGAGGGT	60
CCCTGCTTCT TCCTACAGCC GTTCCGGGC ATG GCC TGG CTG GGG GCG TCG CTC	113
Met Ala Trp Leu Gly Ala Ser Leu	
1 5	
CAC GTC TGG GGT TGG CTA ATG CTC GGC AGC TGC CTC CTG GCC AGA GCC	161
His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala	
10 15 20	
CAG CTG GAT TCT GAT GGC ACC ATC ACT ATA GAG GAG CAG ATT GTC CTT	209
Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu	
25 30 35 40	
GTG CTG AAA GCG AAA GTA CAA TGT GAA CTC AAC ATC ACA GCT CAA CTC	257
Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu	
45 50 55	
CAG GAG GGA GAA GGT AAT TGT TTC CCT GAA TGG GAT GGA CTC ATT TGT	305
Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys	
60 65 70	
TGG CCC AGA GGA ACA GTG GGG AAA ATA TCG GCT GTT CCA TGC CCT CCT	353
Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro	
75 80 85	
TAT ATT TAT GAC TTC AAC CAT AAA GGA GTT GCT TTC CGA CAC TGT AAC	401
Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn	
90 95 100	
CCC AAT GGA ACA TGG GAT TTT ATG CAC AGC TTA AAT AAA ACA TGG GCC	449
Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala	
105 110 115 120	
AAT TAT TCA GAC TGC CTT CGC TTT CTG CAG CCA GAT ATC AGC ATA GGA	497

Asn	Tyr	Ser	Asp	Cys	Leu	Arg	Phe	Leu	Gln	Pro	Asp	Ile	Ser	Ile	Gly	
				125					130					135		
AAG	CAA	GAA	TTC	TGT	GAA	CGC	CTC	TAT	GTA	ATG	TAT	ACC	GTT	GGC	TAC	545
Lys	Gln	Glu	Phe	Cys	Glu	Arg	Leu	Tyr	Val	Met	Tyr	Thr	Val	Gly	Tyr	
			140					145					150			
TCC	ATC	TCT	TTT	GGT	TCC	TTG	GCT	GTG	GCT	ATT	CTC	ATC	ATT	GGT	TAC	593
Ser	Ile	Ser	Phe	Gly	Ser	Leu	Ala	Val	Ala	Ile	Leu	Ile	Ile	Gly	Tyr	
		155					160					165				
TTC	AGA	CGA	TTG	CAT	TGC	ACT	AGG	AAC	TAT	ATC	CAC	ATG	CAC	TTA	TTT	641
Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	
	170					175					180					
GTG	TCT	TTC	ATG	CTG	AGA	GCT	ACA	AGC	ATC	TTT	GTC	AAA	GAC	AGA	GTA	689
Val	Ser	Phe	Met	Leu	Arg	Ala	Thr	Ser	Ile	Phe	Val	Lys	Asp	Arg	Val	
185					190					195					200	
GTC	CAT	GCT	CAC	ATA	GGA	GTA	AAG	GAG	CTG	GAG	TCC	CTA	ATA	ATG	CAG	737
Val	His	Ala	His	Ile	Gly	Val	Lys	Glu	Leu	Glu	Ser	Leu	Ile	Met	Gln	
				205					210					215		
GAT	GAC	CCA	CAA	AAT	TCC	ATT	GAG	GCA	ACT	TCT	GTG	GAC	AAA	TCA	CAA	785
Asp	Asp	Pro	Gln	Asn	Ser	Ile	Glu	Ala	Thr	Ser	Val	Asp	Lys	Ser	Gln	
		220						225					230			
TAT	ATC	GGG	TGC	AAG	ATT	GCT	GTT	GTG	ATG	TTT	ATT	TAC	TTC	CTG	GCT	833
Tyr	Ile	Gly	Cys	Lys	Ile	Ala	Val	Val	Met	Phe	Ile	Tyr	Phe	Leu	Ala	
		235					240					245				
ACA	AAT	TAT	TAT	TGG	ATC	CTG	GTG	GAA	GGT	CTC	TAC	CTG	CAT	AAT	CTC	881
Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Asn	Leu	
	250					255					260					
ATC	TTT	GTG	GCT	TTC	TTT	TCG	GAC	ACC	AAA	TAC	CTG	TGG	GGC	TTC	ATC	929
Ile	Phe	Val	Ala	Phe	Phe	Ser	Asp	Thr	Lys	Tyr	Leu	Trp	Gly	Phe	Ile	
265					270					275					280	
TTG	ATA	GGC	TGG	GGG	TTT	CCA	GCA	GCA	TTT	GTT	GCA	GCA	TGG	GCT	GTG	977
Leu	Ile	Gly	Trp	Gly	Phe	Pro	Ala	Ala	Phe	Val	Ala	Ala	Trp	Ala	Val	
				285					290					295		
GCA	CGA	GCA	ACT	CTG	GCT	GAT	GCG	AGG	TGC	TGG	GAA	CTT	AGT	GCT	GGA	1025
Ala	Arg	Ala	Thr	Leu	Ala	Asp	Ala	Arg	Cys	Trp	Glu	Leu	Ser	Ala	Gly	
			300					305					310			
GAC	ATC	AAG	TGG	ATT	TAT	CAA	GCA	CCG	ATC	TTA	GCA	GCT	ATT	GGG	CTG	1073
Asp	Ile	Lys	Trp	Ile	Tyr	Gln	Ala	Pro	Ile	Leu	Ala	Ala	Ile	Gly	Leu	
		315					320					325				

AAT TTT ATT CTG TTT CTG AAT ACG GTT AGA GTT CTA GCT ACC AAA ATC	1121
Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile	
330 335 340	
TGG GAG ACC AAT GCA GTT GGG CAT GAC ACA AGG AAG CAA TAC AGG AAA	1169
Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys	
345 350 355 360	
CTG GCC AAA TCG ACA CTG GTC CTG GTC CTA GTC TTT GGA GTG CAT TAC	1217
Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr	
365 370 375	
ATC GTG TTC GTG TGC CTG CCT CAC TCC TTC ACT GGG CTC GGG TGG GAG	1265
Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu	
380 385 390	
ATC CGC ATG CAC TGT GAG CTC TTC TTC AAC TCC TTT CAG GGT TTC TTT	1313
Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe	
395 400 405	
GTG TCT ATC ATC TAC TGC TAC TGC AAT GGA GAG GTT CAG GCA GAG GTG	1361
Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val	
410 415 420	
AAG AAG ATG TGG AGT CGG TGG AAT CTC TCC GTG GAC TGG AAA AGG ACA	1409
Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr	
425 430 435 440	
CCG CCA TGT GGC AGC CGC AGA TGC GGC TCA GTG CTC ACC ACC GTG ACG	1457
Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr	
445 450 455	
CAC AGC ACC AGC AGC CAG TCA CAG GTG GCG GCA GCA CAC GCA TGG TGC	1505
His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys	
460 465 470	
TTA TCT CTG GCA AAG CTG CCA AGA TCG CCA GCA GAC AGC CTG ACA GCC	1553
Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala	
475 480 485	
ACA TCA CTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC	1601
Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala	
490 495 500	
TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG	1649
Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln	
505 510 515 520	
AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC	1697
Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn	
525 530 535	

CCA GAC ACT GAA GGA TGACAAGGAG AACTGAGGA TGTTCCTCTGA ATGGACATGT 1752  
 Pro Asp Thr Glu Gly  
 540

GTGGCTGACT TTCATGGGCT GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT 1812

CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTTTA 1872

GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT 1932

AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT 1992

GTGATTGTTC A 2003

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Trp	Leu	Gly	Ala	Ser	Leu	His	Val	Trp	Gly	Trp	Leu	Met	Leu
1				5					10					15	
Gly	Ser	Cys	Leu	Leu	Ala	Arg	Ala	Gln	Leu	Asp	Ser	Asp	Gly	Thr	Ile
			20					25					30		
Thr	Ile	Glu	Glu	Gln	Ile	Val	Leu	Val	Leu	Lys	Ala	Lys	Val	Gln	Cys
			35				40					45			
Glu	Leu	Asn	Ile	Thr	Ala	Gln	Leu	Gln	Glu	Gly	Glu	Gly	Asn	Cys	Phe
	50					55					60				
Pro	Glu	Trp	Asp	Gly	Leu	Ile	Cys	Trp	Pro	Arg	Gly	Thr	Val	Gly	Lys
	65				70					75					80
Ile	Ser	Ala	Val	Pro	Cys	Pro	Pro	Tyr	Ile	Tyr	Asp	Phe	Asn	His	Lys
			85					90					95		
Gly	Val	Ala	Phe	Arg	His	Cys	Asn	Pro	Asn	Gly	Thr	Trp	Asp	Phe	Met
		100					105						110		
His	Ser	Leu	Asn	Lys	Thr	Trp	Ala	Asn	Tyr	Ser	Asp	Cys	Leu	Arg	Phe
		115					120					125			

Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu  
 130 135 140  
 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala  
 145 150 155 160  
 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg  
 165 170 175  
 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr  
 180 185 190  
 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys  
 195 200 205  
 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu  
 210 215 220  
 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val  
 225 230 235 240  
 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val  
 245 250 255  
 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp  
 260 265 270  
 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala  
 275 280 285  
 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala  
 290 295 300  
 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala  
 305 310 315 320  
 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr  
 325 330 335  
 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His  
 340 345 350  
 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu  
 355 360 365  
 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His  
 370 375 380  
 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe  
 385 390 395 400

Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys  
 405 410 415  
 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn  
 420 425 430  
 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys  
 435 440 445  
 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln  
 450 455 460  
 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg  
 465 470 475 480  
 Ser Pro Ala Asp Ser Leu Thr Ala Thr Ser Leu Tyr Leu Ala Met Ser  
 485 490 495  
 Gly Val Thr Gln Ser Arg Thr Ala Ser His Thr Leu Ser Thr Arg Ser  
 500 505 510  
 Asn Lys Glu Asp Ser Gly Arg Gln Arg Asp Asp Ile Leu Met Glu Lys  
 515 520 525  
 Pro Ser Arg Pro Met Glu Ser Asn Pro Asp Thr Glu Gly  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGCCGTCCC GGGCTTGGCC TGG

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCAGTGTC GACTTGTCAT CCTTCAG

27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGGCATAT TGGAAGCTTT TTGCGGG

27

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGTTTCTAG ATGTCATCCT TCAGTGTC

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCTACCCGG GCCGCCATCA TGGCCTGGCT GGGGGGCCT

39

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGTTTCTAG ATGTCATCCT TCAGTGTC

28